What is Claimed is:

1. A method comprising:

    a) attaching one or more template nucleic acid molecules to one or more structures;

    b) synthesizing one or more complementary nucleic acids from labeled nucleotides;

    c) detecting changes in a property of the structures;

    d) identifying the incorporated nucleotides from the changes in a property of the structures; and

    e) determining the sequence of the template nucleic acid.

2. The method of claim 1, wherein the changes in a property of the structures are a function of the mass of the attached nucleic acids.

3. The method of claim 1, wherein the changes in a property of the structures are a function of the surface stress of the structure.

4. The method of claim 1 wherein the structures are cantilevers.

5. The method of claim 1, wherein the changes in a property of the structures are detected by optical beam detection, piezoelectric detection, piezoresistance detection or electrical resistance detection.

6. The method of claim 1, wherein the changes in property of the structures are detected by changes in the resonant frequency of the structures or in the resistance of an electrical circuit associated with the structure.

7. The method of claim 1, wherein the labeled nucleotides comprise at least one mass labeling group.

8. The method of claim 7, wherein each different type of nucleotide comprises a distinguishable mass labeling group.

9. The method of claim 7, wherein the mass labeling groups are selected from the group consisting of nanoparticles, nanoparticle aggregates, carbon nanotubes, fullerenes, functionalized fullerenes, quantum dots, dendrimers, organic molecules, polymers, heavy atoms, fluorescent labels, luminescent labels and mass spectroscopic labels.

10. The method of claim 1, further comprising hybridizing primers to the template nucleic acids.

11. The method of claim 10, wherein the labeled nucleotides are covalently attached to the 3' end of the primer by a polymerase.

12. The method of claim 1, wherein the template nucleic acid molecules are arranged on part of the surface of the structures in a selected pattern.

13. The method of claim 1, wherein only a single type of nucleotide is exposed to the template and complementary nucleic acids at one time.

14. The method of claim 8, wherein four different types of nucleotides are exposed to the template and complementary nucleic acids at the same time.

15. A method for nucleic acid analysis comprising:

a) attaching at least one template nucleic acid to one or more structures;

b) synthesizing at least one complementary nucleic acid segment comprising a selected number of labeled nucleotides;

c) detecting changes in a property of the structures upon incorporation of the labeled nucleotides; and

d) determining the sequence of the nucleic acid segment from the changes in the property of the structures.

16. The method of claim 15, further comprising:

e) replacing the labeled nucleotides in the complementary nucleic acid segment with unlabeled nucleotides;

f) synthesizing an adjacent complementary nucleic acid segment comprising a selected number of labeled nucleotides;

g) detecting changes in a property of the structures upon incorporation of the labeled nucleotides; and

h) determining the sequence of the adjacent complementary nucleic acid segment.

17. The method of claim 16, further comprising repeating (e) through (h) until a nucleic acid sequence is obtained.

18. The method of claim 16, wherein the labeled nucleotides are replaced with unlabeled nucleotides by removing the labels from the labeled nucleotides.

19. The method of claim 15, wherein the structures are cantilevers.

20. The method of claim 19, wherein the property of the structures is a deflection of the cantilevers, a resonant frequency of the cantilevers or the resistance of an electrical circuit associated with the cantilevers.

21. The method of claim 20, wherein a deflection of the cantilevers, a shift in the resonant frequency of the cantilevers or a change in the resistance of an electrical circuit associated with the cantilevers is a function of the mass of the labeled nucleotides.

22. The method of claim 20, wherein a deflection of the cantilevers, a shift in the resonant frequency of the cantilevers or a change in the resistance of an electrical circuit associated with the cantilevers is a function of the surface stress of the cantilever.

23. The method of claim 15, wherein the template nucleic acids are arranged on part of the surface of the structures in a selected pattern.

24. An apparatus comprising:

a) an analysis chamber containing one or more structures;

b) one or more reagent reservoirs in fluid communication with the analysis chamber;

c) a detection unit operably coupled to the structures; and

d) a data processing and control unit.

25. The apparatus of claim 24, further comprising one or more nucleic acids attached to the structures.

26. The apparatus of claim 25, further comprising one or more polymerases in the analysis chamber.

27. The apparatus of claim 24, wherein the structures are cantilevers.

28. The apparatus of claim 24, wherein the detection unit comprises a position sensitive photodetector, a piezoelectric detector or a piezoresistor.

29. The apparatus of claim 24, wherein the detection unit comprises a laser.

30. The apparatus of claim 25, said detection unit to detect changes in mass of nucleic acids attached to said structures and/or the surface stress of said structures.

31. An apparatus comprising:

a) an analysis chamber containing at least one cantilever;

b) one or more nucleic acids molecules attached to the at least one cantilever;

c) a detection unit to detect deflection of the at least one cantilever; and

d) a data processing and control unit.

32. The apparatus of claim 31, further comprising an information processing and control system.

33. The apparatus of claim 32, wherein the information processing and control system is a computer.

34. The apparatus of claim 31, wherein the detection unit comprises a laser and a position sensitive photodetector.

35. The apparatus of claim 31, wherein the detection unit comprises a piezoelectric detector, a piezoresistive detector or a piezomagnetic detector.

36. The apparatus of claim 31, wherein the nucleic acids molecules comprise a template from about 10 to approximately 100,000 nucleotides in length.

37. The apparatus of claim 31, further comprising an array of cantilevers, each associated with the same molecule.

38. The apparatus of claim 31, further comprising an array of cantilevers, each associated with a different molecule.

39. An apparatus comprising:

a) an analysis chamber containing at least one cantilever;

b) one or more nucleic acids molecules attached to the at least one cantilever;

c) a piezoresistive resistor embedded at the fixed end of at least one cantilever;

d) a detection unit to detect deflection of the at least one cantilever; and

e) a data processing and control unit.

40. The apparatus of claim 39, further comprising a resistance measuring device.

41. The apparatus of claim 39, wherein the nucleic acids molecules comprise a template from about 10 to approximately 100,000 nucleotides in length.

42. An apparatus comprising:

a) an analysis chamber containing at least one cantilever;

b) the at least one cantilever coated with a substance;

c) one or more nucleic acids molecules associated with the at least one cantilever;

d) one or more polymerases in the analysis chamber;

e) a detection unit to detect deflection of the at least one cantilever; and

f) a data processing and control unit.

43. The apparatus of claim 42, wherein the substance comprises an alloy.

44. The apparatus of claim 43, wherein the alloy is gold.

45. The apparatus of claim 41, wherein the nucleic acids molecules are anchored to the cantilever through a thiol group.